1646

1600

ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/319,724A

DATE: 01/08/2003
TIME: 14:43:08

Input Set : A:\aoyama5001.ST25.txt
Output Set: N:\CRF4\01082003\I319724A.raw

<110> APPLICANT: VETIGEN
LENZEN, Gerlinde
STROSBERG, Arthur Donny
SUGASAWA, Toshinari
MOROOKA, Shigeaki
<120> TITLE OF INVENTION: MAMMALIAN ICYP (IODOCYANOPINDOLOL) RECEPTOR AND ITS APPLICATIONS
<130> FILE REFERENCE: 053356-5001-US
<140> CURRENT APPLICATION NUMBER: US 09/319,724A
<141> CURRENT FILING DATE: 1999-09-08
<150> PRIOR APPLICATION NUMBER: EP 96402719.7
<151> PRIOR FILING DATE: 1996-12-12
<160> NUMBER OF SEQ ID NOS: 14
<170> SOFTWARE: PatentIn version 3.1
<210> SEQ ID NO: 1
<211> LENGTH: 439
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 1

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Met Tyr Ile Asp Asp Leu Pro Ile Trp Gly Ile Val Gly Glu Ala Asp
1               5                  10                  15
Glu Asn Gly Glu Asp Tyr Tyr Leu Trp Thr Tyr Lys Lys Leu Glu Ile
            20                  25                  30
Gly Phe Asn Gly Asn Arg Ile Val Asp Val Asn Leu Thr Ser Glu Gly
        35                  40                  45
Lys Val Lys Leu Val Pro Asn Thr Lys Ile Gln Met Ser Tyr Ser Val
    50                  55                  60
Lys Trp Lys Lys Ser Asp Val Lys Phe Glu Asp Arg Phe Asp Lys Tyr
65                  70                  75                  80
Leu Asp Pro Ser Phe Phe Gln His Arg Ile His Trp Phe Ser Ile Phe
                85                  90                  95
Asn Ser Phe Met Met Val Ile Phe Leu Val Gly Leu Val Ser Met Ile
            100                 105                 110
Leu Met Arg Thr Leu Arg Lys Asp Tyr Ala Arg Tyr Ser Lys Glu Glu
        115                 120                 125
Glu Met Asp Asp Met Asp Arg Asp Leu Gly Asp Glu Tyr Gly Trp Lys
    130                 135                 140
Gln Val His Gly Asp Val Phe Arg Pro Ser Ser His Pro Leu Ile Phe
145                 150                 155                 160
Ser Ser Leu Ile Gly Ser Gly Cys Gln Ile Phe Ala Val Ser Leu Ile
                165                 170                 175
Val Ile Ile Val Ala Met Ile Glu Asp Leu Tyr Thr Glu Arg Gly Ser
            180                 185                 190
Met Leu Ser Thr Ala Ile Phe Val Tyr Ala Ala Thr Ser Pro Val Asn
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```
79         195                 200                 205
82 Gly Tyr Phe Gly Gly Ser Leu Tyr Ala Arg Gln Gly Gly Arg Arg Trp
83     210                 215                 220
86 Ile Lys Gln Met Phe Ile Gly Ala Phe Leu Ile Pro Ala Met Val Cys
87 225                 230                 235                 240
90 Gly Thr Ala Phe Phe Ile Asn Phe Ile Ala Ile Tyr Tyr His Ala Ser
91                 245                 250                 255
94 Arg Ala Ile Pro Phe Gly Thr Met Val Ala Val Cys Cys Ile Cys Phe
95             260                 265                 270
98 Phe Val Ile Leu Pro Leu Asn Leu Val Gly Thr Ile Leu Gly Arg Asn
99         275                 280                 285
102 Leu Ser Gly Gln Pro Asn Phe Pro Cys Arg Val Asn Ala Val Pro Arg
103     290                 295                 300
106 Pro Ile Pro Glu Lys Lys Trp Phe Met Glu Pro Ala Val Ile Val Cys
107 305                 310                 315                 320
110 Leu Gly Gly Ile Leu Pro Phe Gly Ser Ile Phe Ile Glu Met Tyr Phe
111                 325                 330                 335
114 Ile Phe Thr Ser Phe Trp Ala Tyr Lys Ile Tyr Tyr Val Tyr Gly Phe
115             340                 345                 350
118 Met Met Leu Val Leu Val Ile Leu Cys Ile Val Thr Val Cys Val Thr
119         355                 360                 365
122 Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala Glu Asp Tyr Arg Trp Gln
123     370                 375                 380
126 Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr Ala Ile Tyr Val Tyr Met
127 385                 390                 395                 400
130 Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr Lys Met Tyr Gly Leu Phe
131                 405                 410                 415
134 Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala Val Phe Ser Thr Ala Leu
135             420                 425                 430
138 Gly Ile Met Cys Gly Ala Ile
139         435
142 <210> SEQ ID NO: 2
143 <211> LENGTH: 1317
144 <212> TYPE: DNA
145 <213> ORGANISM: Homo sapiens
147 <400> SEQUENCE: 2
148 atgtacatag atgatttacc aatatggggt attgttggtg aggctgatga aaatggagaa     60
150 gattactatc tttggaccta taaaaaactt gaaataggtt ttaatggaaa tcgaattgtt    120
152 gatgttaatc taactagtga aggaaaggtg aaactggttc caaatactaa aatccagatg    180
154 tcatattcag taaaatggaa aaagtcagat gtgaaatttg aagatcgatt tgacaaatat    240
156 cttgatccgt ccttttttca acatcggatt cattggtttt caattttcaa ctccttcatg    300
158 atggtgatct tcttggtggg cttagtttca atgattttaa tgagaacatt aagaaaagat    360
160 tatgctcggt acagtaaaga ggaagaaatg gatgatatgg atagagacct aggagatgaa    420
162 tatggatgga aacaggtgca tggagatgta tttagaccat caagtcaccc actgatattt    480
164 tcctctctga ttggttctgg atgtcagata tttgctgtgt ctctcatcgt tattattgtt    540
166 gcaatgatag aagatttata tactgagagg ggatcaatgc tcagtacagc catatttgtc    600
168 tatgctgcta cgtctccagt gaatggttat tttggaggaa gtctgtatgc tagacaagga    660
170 ggaaggagat ggataaagca gatgtttatt ggggcattcc ttatcccagc tatggtgtgt    720
172 ggcactgcct tcttcatcaa tttcatagcc atttattacc atgcttcaag agccattcct    780
```

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Input Set : **A:\aoyama5001.ST25.txt**
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```
174 tttggaacaa tggtggccgt ttgttgcatc tgtttttttg ttattcttcc tctaaatctt    840
176 gttggtacaa tacttggccg aaatctgtca ggtcagccca actttccttg tcgtgtcaat    900
178 gctgtgcctc gtcctatacc ggagaaaaaa tggttcatgg agcctgcggt tattgtttgc    960
180 ctgggtggaa ttttaccttt tggttcaatc tttattgaaa tgtatttcat cttcacgtct   1020
182 ttctgggcat ataagatcta ttatgtctat ggcttcatga tgctggtgct ggttatcctg   1080
184 tgcattgtga ctgtctgtgt gactattgtg tgcacatatt ttctactaaa tgcagaagat   1140
186 taccggtggc aatggacaag ttttctctct gctgcatcaa ctgcaatcta tgtttacatg   1200
188 tattcctttt actactattt tttcaaaaca aagatgtatg gcttatttca aacatcattt   1260
190 tactttggat atatggcggt atttagcaca gccttgggga taatgtgtgg agcgatt     1317
193 <210> SEQ ID NO: 3
194 <211> LENGTH: 965
195 <212> TYPE: DNA
196 <213> ORGANISM: Homo sapiens
198 <400> SEQUENCE: 3
199 cagatgtcat attcagtaaa atggaaaaag tcagatgtga aatttgaaga tcgatttgac     60
201 aaatatcttg atccgtcctt ttttcaacat cggattcatt ggttttcaat tttcaactcc    120
203 ttcatgatgg tgatcttctt ggtgggctta gtttcaatga ttttaatgag aacattaaga    180
205 aaagattatg ctcggtacag taaagaggaa gaaatggatg atatggatag agacctagga    240
207 gatgaatatg gatggaaaca ggtgcatgga gatgtattta gaccatcaag tcacccactg    300
209 atattttcct ctctgattgg ttctggatgt cagatatttg ctgtgtctct catcgttatt    360
211 attgttgcaa tgatagaaga tttatatact gagaggggat caatgctcag tacagccata    420
213 tttgtctatg ctgctacgtc tccagtgaat ggttatttta gaggaagtct gtatgctaga    480
215 caaggaggaa ggagatggat aaagcagatg ttattgggg cattccttat cccagctatg    540
217 gtgtgtggca ctgccttctt catcaatttc atagccattt attaccatgc ttcaagagcc    600
219 attccttttg gaacaatggt ggccgtttgt tgcatctgtt tttttgttat tcttcctcta    660
221 aatcttgttg gtacaatact tggccgaaat ctgtcaggtc agcccaactt tccttgtcgt    720
223 gtcaatgctg tgcctcgtcc tataccggag aaaaaatggt tcatggagcc tgcggttatt    780
225 gtttgcctgg gtggaatttt acctttggt tcaatcttta ttgaaatgta tttcatcttc    840
227 acgtctttct gggcatataa gatctattat gtctatggct tcatgatgct ggtgctggtt    900
229 atcctgtgca ttgtgactgt ctgtgtgact attgtgtgca catattttct actaaatgca    960
231 gaaga                                                              965
234 <210> SEQ ID NO: 4
235 <211> LENGTH: 285
236 <212> TYPE: DNA
237 <213> ORGANISM: Homo sapiens
239 <400> SEQUENCE: 4
240 tcagtaaaat ggaaaaagtc agatgtgaaa tttgaagatc gatttgacaa atatcttgat     60
242 ccgtccttt ttcaacatcg gattcattgg ttttcaattt tcaactcctt catgatggtg    120
244 atcttcttgg tgggcttagt ttcaatgatt ttaatgagaa cattaagaaa agattatgct    180
246 cggtacagta aagaggaaga aatggatgat atggatagag acctaggaga tgaatatgga    240
248 tggaaacagg tgcatggaga tgtatttaga ccatcaagtc accca                    285
251 <210> SEQ ID NO: 5
252 <211> LENGTH: 17
253 <212> TYPE: PRT
254 <213> ORGANISM: Artificial sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: Fragment generated by acidic cleavage of polypeptide able to
bind ICYP
259 <400> SEQUENCE: 5
261 Asp Pro Ser Phe Phe Gln His Arg Ile His Trp Phe Ser Ile Phe Asn
```

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262 1 5 10 15
265 Ser
269 <210> SEQ ID NO: 6
270 <211> LENGTH: 17
271 <212> TYPE: PRT
272 <213> ORGANISM: Artificial sequence
274 <220> FEATURE:
275 <223> OTHER INFORMATION: Fragment generated by acidic cleavage of polypeptide able to bind ICYP
277 <220> FEATURE:
278 <221> NAME/KEY: MISC_FEATURE
279 <222> LOCATION: (3)..(3)
280 <223> OTHER INFORMATION: Xaa can by any amino acid
283 <400> SEQUENCE: 6
W--> 285 Asp Pro Xaa Phe Phe Gln His Arg Ile His Val Phe Ser Ile Phe Asn
286 1 5 10 15
289 His
293 <210> SEQ ID NO: 7
294 <211> LENGTH: 20
295 <212> TYPE: DNA
296 <213> ORGANISM: Artificial sequence
298 <220> FEATURE:
299 <223> OTHER INFORMATION: probe/primer
301 <400> SEQUENCE: 7
302 tcagtaaaat ggaaaaagtc 20
305 <210> SEQ ID NO: 8
306 <211> LENGTH: 20
307 <212> TYPE: DNA
308 <213> ORGANISM: Artificial sequence
310 <220> FEATURE:
311 <223> OTHER INFORMATION: probe/primer
313 <400> SEQUENCE: 8
314 tgggtgactt gatggtctaa 20
317 <210> SEQ ID NO: 9
318 <211> LENGTH: 19
319 <212> TYPE: DNA
320 <213> ORGANISM: Artificial sequence
322 <220> FEATURE:
323 <223> OTHER INFORMATION: probe/primer
325 <400> SEQUENCE: 9
326 gctgtgtctc tcatcgtta 19
329 <210> SEQ ID NO: 10
330 <211> LENGTH: 20
331 <212> TYPE: DNA
332 <213> ORGANISM: Artificial sequence
334 <220> FEATURE:
335 <223> OTHER INFORMATION: probe/primer
337 <400> SEQUENCE: 10
338 ccatccatat tcatctccta 20
341 <210> SEQ ID NO: 11

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Input Set : **A:\aoyama5001.ST25.txt**
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```
342 <211> LENGTH: 21
343 <212> TYPE: DNA
344 <213> ORGANISM: Artificial sequence
346 <220> FEATURE:
347 <223> OTHER INFORMATION: probe/primer
349 <400> SEQUENCE: 11
350 cggtatagga cgaggcacag c                                          21
353 <210> SEQ ID NO: 12
354 <211> LENGTH: 18
355 <212> TYPE: DNA
356 <213> ORGANISM: Artificial sequence
358 <220> FEATURE:
359 <223> OTHER INFORMATION: probe/primer
361 <400> SEQUENCE: 12
362 actgaatatg acatctgg                                              18
365 <210> SEQ ID NO: 13
366 <211> LENGTH: 1800
367 <212> TYPE: DNA
368 <213> ORGANISM: Homo sapiens
370 <220> FEATURE:
371 <221> NAME/KEY: CDS
372 <222> LOCATION: (3)..(1730)
373 <223> OTHER INFORMATION:
W--> 375 <400> 13
376 cc gcc gcg ctg tgg ctg ctg ctg ctg ctg ctg ccc cgg acc cgg gcg     47
377    Ala Ala Leu Trp Leu Leu Leu Leu Leu Leu Pro Arg Thr Arg Ala
378    1               5                  10                  15
380 gac gag cac gaa cac acg tat caa gat aaa gag gaa gtt gtc tta tgg     95
381 Asp Glu His Glu His Thr Tyr Gln Asp Lys Glu Glu Val Val Leu Trp
382                 20                  25                  30
384 atg aat act gtt ggg ccc tac cat aat cgt caa gaa aca tat aag tac    143
385 Met Asn Thr Val Gly Pro Tyr His Asn Arg Gln Glu Thr Tyr Lys Tyr
386             35                  40                  45
388 ttt tca ctt cca ttc tgt gtg ggg tca aaa aaa agt atc agt cat tac    191
389 Phe Ser Leu Pro Phe Cys Val Gly Ser Lys Lys Ser Ile Ser His Tyr
390         50                  55                  60
392 cat gaa act ctg gga gaa gca ctt caa ggg gtt gaa ttg gaa ttt agt    239
393 His Glu Thr Leu Gly Glu Ala Leu Gln Gly Val Glu Leu Glu Phe Ser
394     65                  70                  75
396 ggt ctg gat att aaa ttt aaa gat gat gtg atg cca gcc act tac tgt    287
397 Gly Leu Asp Ile Lys Phe Lys Asp Asp Val Met Pro Ala Thr Tyr Cys
398 80                  85                  90                  95
400 gaa att gat tta gat aaa gaa aag aga gat gca ttt gta tat gcc ata    335
401 Glu Ile Asp Leu Asp Lys Glu Lys Arg Asp Ala Phe Val Tyr Ala Ile
402                 100                 105                 110
404 aaa aat cat tac tgg tac cag atg tac ata gat gat tta cca ata tgg    383
405 Lys Asn His Tyr Trp Tyr Gln Met Tyr Ile Asp Asp Leu Pro Ile Trp
406             115                 120                 125
408 ggt att gtt ggt gag gct gat gaa aat gga gaa gat tac tat ctt tgg    431
```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/08/2003
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; Xaa Pos. 3

VERIFICATION SUMMARY DATE: 01/08/2003
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L:285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:375 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:373